usage and the GC content (37%) of the gene were similar to that described for other *H. pylori* genes (13, 26). A putative ribosome binding site: AGGAG, was identified 5 base pairs upstream from the proposed ATG starting codon. Computer search for promoter sequences of the region upstream from the ATG start codon, identified sequences resembling either -10 or -35 regions, however, a region with good consensus to an *E. coli* promoter, or resembling published *H. pylori* promoter sequences was not found. Primer extension analysis of purified *H. pylori* RNA showed that 104 and 214 base pairs upstream from the ATG start codon there are two transcriptional starts sites. Canonical promoters could not be identified upstream from either transcriptional initiation sites. The expression of a portion of the CAI antigen by clone 57/D suggests that *E. coli* is also recognizing a promoter in this region, however, it is not clear whether *E. coli* recognizes the same promoters of *H. pylori* or whether the *H. pylori* DNA that is rich in A-T provides *E. coli* with regions that may act as promoters. A rho independent terminator was identified downstream from the stop codon. In Fig. 4, the AGGAG ribosome binding site and terminator are underlined, and the repeated sequence and motif containing 6 asparagines are boxed. The CAI antigen was very hydrophilic, and did not show obvious leader peptide or transmembrane sequences. The most hydrophilic region was from amino acids 600 to 900, where also a number of unusual features can be observed: the repetition of the sequences EFKNGKNKDFSK (SEQ ID NO:9) and EPIYA (SEQ ID NO:10), and the presence of a stretch of six contiguous asparagines (boxed in Fig. 4).--